=> file medline caplus esbiobase
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	1.47	1.47

FILE 'MEDLINE' ENTERED AT 16:24:39 ON 16 DEC 2002

FILE 'CAPLUS' ENTERED AT 16:24:39 ON 16 DEC 2002
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FILE 'ESBIOBASE' ENTERED AT 16:24:39 ON 16 DEC 2002

=> s (Green (w) fluorescen? or GFP) and (cruzi)
L1 42 (GREEN (W) FLUORESCEN? OR GFP) AND (CRUZI)

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2 20 DUP REM L1 (22 DUPLICATES REMOVED)

=> d 1-20 ti

L2 ANSWER 1 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI Screening method for identifying biological active agents against specific cellular targets

L2 ANSWER 2 OF 20 MEDLINE
TI The Trypanosoma **cruzi** enzyme TcGPXI is a glycosomal peroxidase and can be linked to trypanothione reduction by glutathione or tryparedoxin.

L2 ANSWER 3 OF 20 MEDLINE DUPLICATE 1
TI Regulation of Trypanosoma **cruzi** invasion of nonphagocytic cells by the endocytically active GTPases dynamin, Rab5, and Rab7.

L2 ANSWER 4 OF 20 MEDLINE DUPLICATE 2
TI ORF-FINDER: a vector for high-throughput gene identification.

L2 ANSWER 5 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI Clk-2, cex-7 and coq-4 genes and physiological function in developmental rate and longevity and use in drug screening

L2 ANSWER 6 OF 20 MEDLINE DUPLICATE 3
TI TcSCA complements yeast mutants defective in Ca2+ pumps and encodes a Ca2+-ATPase that localizes to the endoplasmic reticulum of Trypanosoma **cruzi**.

L2 ANSWER 7 OF 20 MEDLINE DUPLICATE 4
TI Simultaneous stable expression of neomycin phosphotransferase and **green fluorescence** protein genes in Trypanosoma **cruzi**.

L2 ANSWER 8 OF 20 MEDLINE DUPLICATE 5
TI Import of proteins into the trypanosome nucleus and their distribution at karyokinesis.

L2 ANSWER 9 OF 20 MEDLINE DUPLICATE 6
TI A new developmentally regulated gene family in Leishmania amastigotes encoding a homolog of amastin surface proteins.

L2 ANSWER 10 OF 20 MEDLINE DUPLICATE 7
TI The use of the **green fluorescent** protein to monitor and improve transfection in Trypanosoma **cruzi**.

L2 ANSWER 11 OF 20 MEDLINE DUPLICATE 8
TI Colony polymerase chain reaction of stably transfected trypanosoma **cruzi** grown on solid medium.

L2 ANSWER 12 OF 20 MEDLINE DUPLICATE 9
TI Double-stranded RNA interference in Trypanosoma brucei using head-to-head promoters.

L2 ANSWER 13 OF 20 MEDLINE DUPLICATE 10
TI Protease trafficking in two primitive eukaryotes is mediated by a prodomain protein motif.

L2 ANSWER 14 OF 20 MEDLINE DUPLICATE 11
TI A cell surface mucin specifically expressed in the midgut of the malaria mosquito Anopheles gambiae.

L2 ANSWER 15 OF 20 MEDLINE
TI Flagellar protein localization mediated by a calcium-myristoyl/palmitoyl switch mechanism.

L2 ANSWER 16 OF 20 MEDLINE DUPLICATE 12
TI Expression of a marker for intracellular Trypanosoma **cruzi** amastigotes in extracellular spheromastigotes.

L2 ANSWER 17 OF 20 MEDLINE DUPLICATE 13
TI Expression of Trypanosoma **cruzi** surface antigen FL-160 is controlled by elements in the 3' untranslated, the 3' intergenic, and the coding regions.

L2 ANSWER 18 OF 20 MEDLINE
TI Fluorescence of chromatin DNA by an oxazolium scintillator.

L2 ANSWER 19 OF 20 MEDLINE
TI Fluorescence reaction of chromatin by curcumin.

L2 ANSWER 20 OF 20 CAPLUS COPYRIGHT 2002 ACS
TI Significance of methyl groups on the nucleus of several chemotherapeutic compounds in the 4-aminoquinoline series

=> d 15-19 bib ab

L2 ANSWER 15 OF 20 MEDLINE
AN 1999221641 MEDLINE
DN 99221641 PubMed ID: 10205160
TI Flagellar protein localization mediated by a calcium-myristoyl/palmitoyl switch mechanism.
AU Godsel L M; Engman D M
CS Departments of Microbiology-Immunology and Pathology, Northwestern University Medical School, Chicago, IL 60611, USA.
SO EMBO JOURNAL, (1999 Apr 15) 18 (8) 2057-65.
Journal code: 8208664. ISSN: 0261-4189.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199906

ED Entered STN: 19990628
Last Updated on STN: 19990628
Entered Medline: 19990611

AB The mechanisms by which proteins are targeted to flagella and cilia are poorly understood. We set out to determine the basis for the specific localization of a 24 kDa flagellar calcium-binding protein (FCaBP) expressed in all life cycle stages of Trypanosoma **cruzi**. Through the study of trypanosome transfectants expressing various FCaBP deletion mutants, we found that the N-terminal 24 amino acids of the protein are necessary and sufficient for flagellar localization. Subsequent experiments revealed that FCaBP is myristoylated and palmitoylated and, in fact, is one of very few proteins in the cell possessing these acyl modifications. Both fatty acids are required for flagellar localization, suggesting that FCaBP localization may be mediated through association with the flagellar plasma membrane. Indeed, FCaBP associates with the flagellar membrane in a calcium-dependent manner, reminiscent of the recoverin family of calcium-myristoyl switch proteins. Thus, FCaBP is a novel member of the calcium-acyl switch protein family and is the only member described to date that requires two fatty acid modifications for specific membrane association. Its unique localization mechanism is the first described for any flagellar protein. The existence of such a protein in this protozoan suggests that acylation and calcium switch mechanisms for regulated membrane association are conserved among eukaryotes.

DUPLICATE 12

L2 ANSWER 16 OF 20 MEDLINE
AN 1999178479 MEDLINE
DN 99178479 PubMed ID: 10080394
TI Expression of a marker for intracellular Trypanosoma **cruzi** amastigotes in extracellular spheromastigotes.
AU Teixeira S M; Otsu K; Hill K L; Kirchhoff L V; Donelson J E
CS Department of Internal Medicine, University of Iowa, 52245, USA.
NC AI09872 (NIAID)
AI40591 (NIAID)
SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1999 Jan 25) 98 (2) 265-70.
Journal code: 8006324. ISSN: 0166-6851.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199905
ED Entered STN: 19990517
Last Updated on STN: 19990517
Entered Medline: 19990504

DUPLICATE 13

L2 ANSWER 17 OF 20 MEDLINE
AN 1999404826 MEDLINE
DN 99404826 PubMed ID: 10477176
TI Expression of Trypanosoma **cruzi** surface antigen FL-160 is controlled by elements in the 3' untranslated, the 3' intergenic, and the coding regions.
AU Weston D; La Flamme A C; Van Voorhis W C
CS Department of Medicine, University of Washington, Seattle 98195, USA.
NC F32 AI09235 (NIAID)
R21 AI38924 (NIAID)
SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1999 Jul 30) 102 (1) 53-66.
Journal code: 8006324. ISSN: 0166-6851.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF080220; GENBANK-AF091835; GENBANK-AF091836; GENBANK-X70948
EM 199912

ED Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991221

AB The FL-160 surface antigen gene family of T. **cruzi** consists of hundreds of members of 160 kDa glycoproteins expressed in trypomastigotes, but not in epimastigotes. Steady-state levels of FL-160 mRNA were 80 to 100-fold higher in trypomastigotes than in epimastigotes, yet transcription rates were equivalent between the lifecycle stages. Luciferase reporter constructs demonstrated that the 3' untranslated region (UTR) and intergenic region (IR) following the coding sequence of FL-160 was sufficient to generate 8-fold higher luciferase expression in trypomastigotes compared with epimastigotes. Transfection of 3' UTR/IR deletion constructs revealed cis-acting elements which conferred a trypomastigote-specific expression pattern similar to that of FL-160. Parasites treated with translation and transcription inhibitors, cyclohexamide and Actinomycin D, respectively, displayed a stage-specific pattern of FL-160 mRNA degradation. Epimastigotes, but not trypomastigotes, treated with the inhibitors accumulated a 1.4 Kb FL-160 cleavage product. The cleavage site mapped to a 31 base poly-purine tract in the FL-160 coding region. The first 526 aa of FL-160, containing the 31 base poly-purine tract and several smaller tracts, were fused to **green fluorescent** protein (**GFP**) and expressed from the T. **cruzi** tubulin locus. Stable transformants expressed 4-fold more FL-160:**GFP** fusion mRNA and 12-fold more fusion protein in the trypomastigote stage than in the epimastigote stage suggesting post-transcriptional and translational control elements. These data reveal at least two distinct control mechanisms for trypomastigote-specific expression of FL-160 surface glycoproteins, one involving the 3' UTR/IR and one involving the coding region of FL-160.

L2 ANSWER 18 OF 20 MEDLINE
AN 93039206 MEDLINE
DN 93039206 PubMed ID: 1418244
TI Fluorescence of chromatin DNA by an oxazolium scintillator.
AU Stockert J C
CS Max-Planck-Institut fur Biologie, Abteilung Mikrobiologie, Tubingen, Bundesrepublik Deutschland.
SO ZEITSCHRIFT FUR NATURFORSCHUNG. SECTION C. JOURNAL OF BIOSCIENCES, (1992 May-Jun) 47 (5-6) 481-2.
Journal code: 8912155. ISSN: 0341-0382.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199212
ED Entered STN: 19930122
Last Updated on STN: 19930122
Entered Medline: 19921204

AB Aqueous solutions of a yellow and highly fluorescent derivative from dimethyl-POPOP, obtained by treating a chloroform solution of this oxazole scintillator with dimethylsulfate, induce a strong blue-green or yellow-**green fluorescence** in chromatin DNA under ultraviolet (365 nm) or violet-blue (436 nm) excitation, respectively. It is suggested that this new and selective fluorescence reaction could originate from binding of the oxazolium derivative into the minor groove of DNA.

L2 ANSWER 19 OF 20 MEDLINE
AN 89302314 MEDLINE
DN 89302314 PubMed ID: 2663005
TI Fluorescence reaction of chromatin by curcumin.
AU Stockert J C; Del Castillo P; Gomez A; Llorente A R
CS Departamento de Biologia, Facultad de Ciencias, Universidad Autonoma de

Madrid, Spain.
SO ZEITSCHRIFT FUR NATURFORSCHUNG. SECTION C. JOURNAL OF BIOSCIENCES, (1989 Mar-Apr) 44 (3-4) 327-9.
Journal code: 8912155. ISSN: 0341-0382.
CY GERMANY, WEST: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198908
ED Entered STN: 19900309
Last Updated on STN: 19900309
Entered Medline: 19890825
AB Treatment of cell smears, paraffin, and Epon tissue sections with aqueous solutions of curcumin results in a **green fluorescence** reaction in chromatin under violet-blue excitation which is abolished after extraction procedures with DNase and TCA. The selective fluorescence characteristics of curcumin support the possibility of employing this dye as a new fluorochrome.

=> FIL STNGUIDE

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	10.86	12.33

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FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Dec 13, 2002 (20021213/UP).

=> s (Green (w) fluorescen? or GFP) (9a) frame#
0 GREEN
1 FLUORESCEN?
0 GFP
4 FRAME#
L3 0 (GREEN (W) FLUORESCEN? OR GFP) (9A) FRAME#

=> file medline caplus esbiobase

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.36	12.69

FILE 'MEDLINE' ENTERED AT 16:31:56 ON 16 DEC 2002

FILE 'CAPLUS' ENTERED AT 16:31:56 ON 16 DEC 2002
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=> s (Green (w) fluorescen? or GFP) (9a) frame#
L4 200 (GREEN (W) FLUORESCEN? OR GFP) (9A) FRAME#

=> s l4 (9a) (out)
L5 7 L4 (9A) (OUT)

=> dup rem l5

PROCESSING COMPLETED FOR L5
L6 3 DUP REM L5 (4 DUPLICATES REMOVED)

=> d 1-3 bib ab

DUPLICATE 1

L6 ANSWER 1 OF 3 MEDLINE
AN 2002654021 IN-PROCESS
DN 22301365 PubMed ID: 12414628
TI Mutations in tetranucleotide repeats following DNA damage depend on repeat sequence and carcinogenic agent.
AU Slebos Robbert J C; Oh Daniel S; Umbach David M; Taylor Jack A
CS Laboratory of Molecular Carcinogenesis, National Institute of Environmental Health Sciences, NIH, Research Triangle Park, North Carolina 27709, USA.. slebos@niehs.nih.gov
SO CANCER RESEARCH, (2002 Nov 1) 62 (21) 6052-60.
Journal code: 2984705R. ISSN: 0008-5472.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS IN-PROCESS; NONINDEXED; Priority Journals
ED Entered STN: 20021105
Last Updated on STN: 20021211
AB Sporadic microsatellite mutations are frequently observed in lung, bladder, and head and neck tumors with intact DNA mismatch repair. AAAG tetranucleotide repeats appear to be especially prone to the accumulation of these mutations. We hypothesized that occurrences of microsatellite mutations in these cancers may be linked to DNA damage caused by exposure to carcinogens in tobacco smoke. To test this hypothesis, we developed a model system based on reactivation of green fluorescent protein (GFP) in which a plasmid vector carries a microsatellite repeat that places the **GFP** sequence **out** of **frame** for protein translation. In this reporter system, DNA slippage mutations can restore the GFP reading frame and become detectable by flow cytometry as GFP-positive cells. Pools of stably transfected RKO cells were treated at four dose levels each of gamma-irradiation, benzo(a)pyrene diol epoxide, N-methyl-N-nitro-N-nitrosoguanidine (MNNG), t-butyl hydrogen peroxide, and UV irradiation and assayed for GFP-positive cells 48 h later. We studied the microsatellite repeats AAAG, ATAG, CAGT, and CA, as well as a control sequence lacking any repetitive elements. A log-linear regression approach was used to discriminate between the effects of repeat unit and dose for each agent. A statistically significant increase in GFP-positive cells was found with increasing dose with all agents, although repeat unit-specific response patterns were only observed with MNNG, t-butyl hydrogen peroxide, and UV irradiation. With MNNG, significant differences in response were observed between dinucleotide and tetranucleotide repeat units. The effects of UV irradiation were consistent with the predicted number of pyrimidine dimers/repeat unit, with higher GFP activation in repeats that had large numbers of adjacent pyrimidines. We found no evidence to indicate that the AAAG repeat responded to any of the DNA-damaging agents with higher levels of GFP activation than other repeat units. These results provide evidence that DNA damage can induce slippage mutations and increase mutation rates in repeated sequences and that there are sequence-specific responses to different types of DNA damage. Our results are compatible with the hypothesis that sporadic microsatellite mutations in human cancer may reflect DNA damage caused by carcinogen exposure.

DUPLICATE 2

L6 ANSWER 2 OF 3 MEDLINE
AN 2002087382 MEDLINE
DN 21673986 PubMed ID: 11814675
TI ORF-FINDER: a vector for high-throughput gene identification.
AU Rombel Irene T; Sykes Kathryn F; Rayner Simon; Johnston Stephen Albert
CS Center for Biomedical Inventions, Department of Internal Medicine,

University of Texas-Southwestern Medical Center, 5323 Harry Hines Boulevard, Dallas, TX 75390-9185, USA.. irene.rombel@utsouthwestern.edu

SO GENE, (2002 Jan 9) 282 (1-2) 33-41.
Journal code: 7706761. ISSN: 0378-1119.

CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200203
ED Entered STN: 20020130
Last Updated on STN: 20020403
Entered Medline: 20020328

AB We have developed a simple and efficient system (ORF-FINDER) for selecting open reading frames (ORFs) from randomly fragmented genomic DNA fragments. The ORF-FINDER vectors are plasmids that contain a translational start site **out** of **frame** with respect to the gene for **green fluorescent** protein (**GFP**). Insertion of DNA fragments that bring the initiating ATG in frame with GFP and that contain no stop codons (that is, ORFs) results in the expression of ORF-GFP fusion proteins. In addition, we have developed software (GeneWorks and GenomeAnalyzer) to predict the optimal insert size for maximizing the number of gene-coding ORFs and minimizing unintentionally selected non-coding ORFs. To demonstrate the feasibility of using the ORF-FINDER system to screen genomes for ORFs, we cloned yeast genomic DNA and succeeded in enriching for ORFs by 25-fold. Furthermore, we have shown that the vector can effectively isolate ORFs from the more complex genomes of eukaryotic parasites. We envision that ORF-FINDER will have several applications including genome sequencing projects, gene building from oligonucleotides and construction of expression libraries enriched for ORFs.

L6 ANSWER 3 OF 3 MEDLINE
AN 2001269925 MEDLINE
DN 21264718 PubMed ID: 11160123
TI Identification of an internal gene to the human Galectin-3 gene with two different overlapping reading frames that do not encode Galectin-3.
AU Guittaut M; Charpentier S; Normand T; Dubois M; Raimond J; Legrand A
CS Centre de Biophysique Moleculaire (affiliated with the University of Orleans), CNRS UPR4301, Rue Charles Sadron, 45071 Orleans Cedex 02, France.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (2001 Jan 26) 276 (4) 2652-7.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF266280
EM 200106
ED Entered STN: 20010625
Last Updated on STN: 20010625
Entered Medline: 20010621

AB We previously reported that alternative transcripts were initiated within the second intron of the human Galectin-3 gene (LGALS3). We now demonstrate that these transcripts arise from an internal gene embedded within LGALS3 and named galig (Galectin-3 internal gene). Tissue-specific expression of galig was assayed by screening of several human tissues. Contrary to LGALS3, galig appears to be tightly regulated and principally activated in leukocytes from peripheral blood. Cloning and characterization of galig transcripts revealed that they contain two **out**-of-frame overlapping open-reading **frames** (ORFs). Transfection of expression vectors encoding enhanced **green fluorescent** protein (EGFP) chimeras indicated that both ORFs could

be translated in proteins unrelated to Galectin-3. The ORF1 polypeptide targets EGFP to cytosol and nucleus whereas ORF2 targets EGFP to mitochondria. These results revealed the exceptional genetic organization of the LGALS3 locus.

=> d his

(FILE 'HOME' ENTERED AT 16:20:47 ON 16 DEC 2002)

FILE 'MEDLINE, CAPLUS, ESBIOBASE' ENTERED AT 16:24:39 ON 16 DEC 2002
L1 42 S (GREEN (W) FLUORESCEN? OR GFP) AND (CRUZI)
L2 20 DUP REM L1 (22 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 16:28:05 ON 16 DEC 2002
L3 0 S (GREEN (W) FLUORESCEN? OR GFP) (9A) FRAME#

FILE 'MEDLINE, CAPLUS, ESBIOBASE' ENTERED AT 16:31:56 ON 16 DEC 2002
L4 200 S (GREEN (W) FLUORESCEN? OR GFP) (9A) FRAME#
L5 7 S L4 (9A) (OUT)
L6 3 DUP REM L5 (4 DUPLICATES REMOVED)

=> dup rem l4
PROCESSING COMPLETED FOR L4
L7 84 DUP REM L4 (116 DUPLICATES REMOVED)

=> s l7 and py<1999
L8 19 L7 AND PY<1999

=> d 1-19 ti

L8 ANSWER 1 OF 19 MEDLINE
TI Libraries of green fluorescent protein fusions generated by transposition in vitro.

L8 ANSWER 2 OF 19 MEDLINE
TI Detection of targeted GFP-Hox gene fusions during mouse embryogenesis.

L8 ANSWER 3 OF 19 MEDLINE
TI UGA codon position affects the efficiency of selenocysteine incorporation into glutathione peroxidase-1.

L8 ANSWER 4 OF 19 MEDLINE
TI Functional regions of the human cytomegalovirus protein pUL97 involved in nuclear localization and phosphorylation of ganciclovir and pUL97 itself.

L8 ANSWER 5 OF 19 MEDLINE
TI Circular mRNA can direct translation of extremely long repeating-sequence proteins in vivo.

L8 ANSWER 6 OF 19 MEDLINE
TI Incorporation of the green fluorescent protein into the herpes simplex virus type 1 capsid.

L8 ANSWER 7 OF 19 MEDLINE
TI Rapid expression screening of Caenorhabditis elegans homeobox open reading **frames** using a two-step polymerase chain reaction promoter-**gfp** reporter construction technique.

L8 ANSWER 8 OF 19 MEDLINE
TI Induced expression of the Candida albicans multidrug resistance gene CDR1 in response to fluconazole and other antifungals.

L8 ANSWER 9 OF 19 MEDLINE
TI Mapping the interacting domains between the rabies virus polymerase and phosphoprotein.

L8 ANSWER 10 OF 19 MEDLINE
TI Expression of foreign proteins by poliovirus polyprotein fusion: analysis of genetic stability reveals rapid deletions and formation of cardioviruslike open reading frames.

L8 ANSWER 11 OF 19 MEDLINE
TI Application of a chimeric green fluorescent protein to study protein-protein interactions.

L8 ANSWER 12 OF 19 MEDLINE
TI Gene trapping with GFP: the isolation of developmental mutants in the slime mold Polysphondylium.

L8 ANSWER 13 OF 19 MEDLINE
TI Structural determinants for the intracellular localization of the isozymes of mammalian hexokinase: intracellular localization of fusion constructs incorporating structural elements from the hexokinase isozymes and the green fluorescent protein.

L8 ANSWER 14 OF 19 MEDLINE
TI Novel green fluorescent protein (GFP) baculovirus expression vectors.

L8 ANSWER 15 OF 19 MEDLINE
TI Gene structure, promoter activity, and chromosomal location of the DR-nm23 gene, a related member of the nm23 gene family.

L8 ANSWER 16 OF 19 MEDLINE
TI Inhibition of viral replication by genetically engineered mutants of the duck hepatitis B virus core protein.

L8 ANSWER 17 OF 19 MEDLINE
TI Use of green fluorescent protein for visualization of cell-specific gene expression and subcellular protein localization during sporulation in Bacillus subtilis.

L8 ANSWER 18 OF 19 CAPLUS COPYRIGHT 2002 ACS
TI Gene trapping with GFP: the isolation of developmental mutants in the slime mold Polysphondylium

L8 ANSWER 19 OF 19 CAPLUS COPYRIGHT 2002 ACS
TI Application of a chimeric green fluorescent protein to study protein-protein interactions

=> d 1, 7,

L8 ANSWER 1 OF 19 MEDLINE
AN 1999051331 MEDLINE
DN 99051331 PubMed ID: 9831655
TI Libraries of green fluorescent protein fusions generated by transposition in vitro.
AU Merkulov G V; Boeke J D
CS Department of Molecular Biology and Genetics, Johns Hopkins University School of Medicine, Baltimore, MD 21205, USA.
NC CA77812 (NCI)
GM36481 (NIGMS)
SO GENE, **(1998 Nov 19)** 222 (2) 213-22.

Journal code: 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199901
ED Entered STN: 19990202
Last Updated on STN: 19990202
Entered Medline: 19990121

L8 ANSWER 7 OF 19 MEDLINE
AN 1998326318 MEDLINE
DN 98326318 PubMed ID: 9661672
TI Rapid expression screening of Caenorhabditis elegans homeobox open reading **frames** using a two-step polymerase chain reaction promoter-**gfp** reporter construction technique.
AU Cassata G; Kagoshima H; Pretot R F; Aspock G; Niklaus G; Burglin T R
CS Department of Cell Biology, University of Basel, Switzerland.
SO GENE, **(1998 May 28)** 212 (1) 127-35.
Journal code: 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199807
ED Entered STN: 19980811
Last Updated on STN: 19980811
Entered Medline: 19980727

=> d 1, 7 bib ab

L8 ANSWER 1 OF 19 MEDLINE
AN 1999051331 MEDLINE
DN 99051331 PubMed ID: 9831655
TI Libraries of green fluorescent protein fusions generated by transposition in vitro.
AU Merkulov G V; Boeke J D
CS Department of Molecular Biology and Genetics, Johns Hopkins University School of Medicine, Baltimore, MD 21205, USA.
NC CA77812 (NCI)
GM36481 (NIGMS)
SO GENE, **(1998 Nov 19)** 222 (2) 213-22.
Journal code: 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199901
ED Entered STN: 19990202
Last Updated on STN: 19990202
Entered Medline: 19990121
AB Two artificial transposons have been constructed that carry a gene encoding Green Fluorescent Protein and can be used for generating libraries of GFP fusions in a gene of interest. One such element, AT2GFP, can be used to generate **GFP** insertions in **frame** with the amino acid sequence of the protein of interest, with a stop codon at the end of the GFP coding sequence; AT2GFP also contains a selectable marker that confers trimethoprim resistance in bacteria. The second element, GS, can be used to generate tribrid GFP fusions because there is no stop codon in the GFP transposon, and the resulting fusion proteins contain the entire amino acid sequence encoded by the gene. The GS element

consists of a **gfp** open reading **frame** and a supF amber suppressor tRNA gene; the supF portion of the GS transposon can be utilized as a selectable marker in bacteria. Its sequence contains a fortuitous open reading **frame**, and thus it can be translated continuously with the **gfp** amino acid sequence. As a target for GFP insertions, we used a plasmid carrying the native Ty1 retrotransposon of the yeast Sacharomyces cerevisiae. The resulting multiple GFP fusions to Ty1 capsid protein Gag and Ty1 integrase were useful in determining the cellular localization of these proteins. Libraries of GFP fusions generated by transposition in vitro represent a novel and potentially powerful method to study the cell distribution and cellular localization signals of proteins.

L8 ANSWER 7 OF 19 MEDLINE
AN 1998326318 MEDLINE
DN 98326318 PubMed ID: 9661672
TI Rapid expression screening of Caenorhabditis elegans homeobox open reading **frames** using a two-step polymerase chain reaction promoter-**gfp** reporter construction technique.
AU Cassata G; Kagoshima H; Pretot R F; Aspock G; Niklaus G; Burglin T R
CS Department of Cell Biology, University of Basel, Switzerland.
SO GENE, **(1998 May 28)** 212 (1) 127-35.
Journal code: 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199807
ED Entered STN: 19980811
Last Updated on STN: 19980811
Entered Medline: 19980727
AB In this paper a description is given of the expression pattern of the Caenorhabditis elegans homeobox gene ceh-38 using GFP reporter constructs, which were generated using a two-step polymerase chain reaction (PCR) procedure. This method allows fast analysis of genes of interest by looking at their expression in vivo using their putative promoter region to control the expression of a reporter gene. In this case the method was applied to screen C. elegans homeobox-containing genes to identify those that are expressed in the head and nervous system. The C. elegans genome project has made rapid progress, and more than 79 megabases of genomic data with several thousand open reading frames are available. This information can be used to design primers from putative promoter regions, which are amplified using long-range PCR. The long-range PCR product is then directly joined to the vector in a long-range Fill-in PCR. Since many genome projects are advancing rapidly, this approach should also be applicable for other model systems, and the method lends itself to automation, since no gel-purification steps are necessary. ceh-38 is a member of the ONECUT class of homeobox genes. Expression of ceh-38 starts during embryogenesis. In larvae and adults, expression was seen in many different types of tissues, such as the pharynx, gut, hypodermis and many nerve cells.

=> FIL STNGUIDE

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	20.65	33.34

FILE 'STNGUIDE' ENTERED AT 16:42:06 ON 16 DEC 2002

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FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Dec 13, 2002 (20021213/UP).

=> d his

     (FILE 'HOME' ENTERED AT 16:20:47 ON 16 DEC 2002)

     FILE 'MEDLINE, CAPLUS, ESBIOBASE' ENTERED AT 16:24:39 ON 16 DEC 2002
L1            42 S (GREEN (W) FLUORESCEN? OR GFP) AND (CRUZI)
L2            20 DUP REM L1 (22 DUPLICATES REMOVED)

     FILE 'STNGUIDE' ENTERED AT 16:28:05 ON 16 DEC 2002
L3             0 S (GREEN (W) FLUORESCEN? OR GFP) (9A) FRAME#

     FILE 'MEDLINE, CAPLUS, ESBIOBASE' ENTERED AT 16:31:56 ON 16 DEC 2002
L4           200 S (GREEN (W) FLUORESCEN? OR GFP) (9A) FRAME#
L5             7 S L4 (9A) (OUT)
L6             3 DUP REM L5 (4 DUPLICATES REMOVED)
L7            84 DUP REM L4 (116 DUPLICATES REMOVED)
L8            19 S L7 AND PY<1999

     FILE 'STNGUIDE' ENTERED AT 16:42:06 ON 16 DEC 2002

=> file medlin biosis caplus
COST IN U.S. DOLLARS                          SINCE FILE      TOTAL
                                                 ENTRY    SESSION
FULL ESTIMATED COST                               0.18      33.52

FILE 'MEDLINE' ENTERED AT 16:43:49 ON 16 DEC 2002

FILE 'BIOSIS' ENTERED AT 16:43:49 ON 16 DEC 2002
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=> s (Green (w) fluorescen? or GFP) and (not or out) (4a) frame#
MISSING TERM 'AND (NOT'
The search profile entered contains a left parenthesis,
'(' followed by an operator.

=> s (Green (w) fluorescen? or GFP) and ("not" or out) (4a) frame#
L9            18 (GREEN (W) FLUORESCEN? OR GFP) AND ("NOT" OR OUT) (4A) FRAME#

=> dup rem l9
PROCESSING COMPLETED FOR L9
L10            7 DUP REM L9 (11 DUPLICATES REMOVED)

=> d 1-7 ti

L10  ANSWER 1 OF 7     MEDLINE                                  DUPLICATE 1
TI   Mutations in tetranucleotide repeats following DNA damage depend on repeat
     sequence and carcinogenic agent.

L10  ANSWER 2 OF 7     MEDLINE                                  DUPLICATE 2
TI   Generation of multiple isoforms of eukaryotic translation initiation
     factor 4GI by use of alternate translation initiation codons.

L10  ANSWER 3 OF 7     MEDLINE                                  DUPLICATE 3
```

TI ORF-FINDER: a vector for high-throughput gene identification.

L10 ANSWER 4 OF 7 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 4
TI DNA vector for determining the presence of **out**-of-reading-**frame** mutations.

L10 ANSWER 5 OF 7 MEDLINE DUPLICATE 5
TI Identification of an internal gene to the human Galectin-3 gene with two different overlapping reading frames that do not encode Galectin-3.

L10 ANSWER 6 OF 7 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Genetic and biochemical characterization of a deletional mutation of the extra-cellular domain of the human G-CSF receptor in a child with severe congenital neutropenia unresponsive to neupogen.

L10 ANSWER 7 OF 7 MEDLINE DUPLICATE 6
TI Random **GFP**::cDNA fusions enable visualization of subcellular structures in cells of Arabidopsis at a high frequency.

=> d 4-7 bib ab

L10 ANSWER 4 OF 7 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 4
AN 2001:508428 BIOSIS
DN PREV200100508428
TI DNA vector for determining the presence of **out**-of-reading-**frame** mutations.
AU Litman, Gary W. (1); Hawke, Noel A.; Haire, Robert N.; Strong, Scott J.
CS (1) Clearwater, FL USA
ASSIGNEE: University of South Florida
PI US 6284496 September 04, 2001
SO Official Gazette of the United States Patent and Trademark Office Patents, (Sep. 4, 2001) Vol. 1250, No. 1, pp. No Pagination. e-file.
ISSN: 0098-1133.
DT Patent
LA English
AB A DNA expression vector for positively selecting in-**frame** or **out**-of-reading-**frame** mutations in DNA sequences to be tested comprising a promotor operatively linked to an expressible reporter gene through a linkage sequence is disclosed. The linkage sequence includes at least two restriction sites and an engineered frameshift mutation. In an embodiment the frameshift is established by complementary sequences SEQ ID Nos:1 and 2. The expressible reporter gene is expressed as a fusion product including a **green fluorescent** protein and the promoter can be lacZ and inducible in E. coli.

L10 ANSWER 5 OF 7 MEDLINE DUPLICATE 5
AN 2001269925 MEDLINE
DN 21264718 PubMed ID: 11160123
TI Identification of an internal gene to the human Galectin-3 gene with two different overlapping reading frames that do not encode Galectin-3.
AU Guittaut M; Charpentier S; Normand T; Dubois M; Raimond J; Legrand A
CS Centre de Biophysique Moleculaire (affiliated with the University of Orleans), CNRS UPR4301, Rue Charles Sadron, 45071 Orleans Cedex 02, France.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (2001 Jan 26) 276 (4) 2652-7.
Journal code: 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF266280

EM 200106
ED Entered STN: 20010625
Last Updated on STN: 20010625
Entered Medline: 20010621
AB We previously reported that alternative transcripts were initiated within the second intron of the human Galectin-3 gene (LGALS3). We now demonstrate that these transcripts arise from an internal gene embedded within LGALS3 and named galig (Galectin-3 internal gene). Tissue-specific expression of galig was assayed by screening of several human tissues. Contrary to LGALS3, galig appears to be tightly regulated and principally activated in leukocytes from peripheral blood. Cloning and characterization of galig transcripts revealed that they contain two **out**-of-**frame** overlapping open-reading frames (ORFs). Transfection of expression vectors encoding enhanced **green fluorescent** protein (EGFP) chimeras indicated that both ORFs could be translated in proteins unrelated to Galectin-3. The ORF1 polypeptide targets EGFP to cytosol and nucleus whereas ORF2 targets EGFP to mitochondria. These results revealed the exceptional genetic organization of the LGALS3 locus.

L10 ANSWER 6 OF 7 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2002:209848 BIOSIS
DN PREV200200209848
TI Genetic and biochemical characterization of a deletional mutation of the extra-cellular domain of the human G-CSF receptor in a child with severe congenital neutropenia unresponsive to neupogen.
AU Sinha, Srish (1); Watkins, Simon; Corey, Seth J. (1)
CS (1) Pediatrics, Children's Hosp of Pittsburgh, Pittsburgh, PA USA
SO Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 440a. http://www.bloodjournal.org/. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December 07-11, 2001
ISSN: 0006-4971.
DT Conference
LA English
AB Severe congenital neutropenia (SCN) is likely to be a multi-factorial disease characterized by a severe reduction in circulating neutrophils. Mutations in the G-CSF Receptor (G-CSFR) or Neutrophil Elastase genes have been found in patients with SCN. Typically, bone marrow aspirates show maturation arrest at the promyelocyte st age. Most patients with SCN respond to G-CSF (Neupogen) with normal neutrophil counts and an excellent quality of life. A few patients, however, do not respond to super-pharmacologic doses of G-CSF. Here, we report a 4 year-old girl with SCN who did not respond to Neupogen (apprx80 ug/kg/d). We hypothesized that there was a defect in the extra-celluar domain of the G-CSFR. RT-PCR was performed on bone marrow-derived mononuclear cells. This showed presence of a wild-type and a shorter transcript. Sequencing revealed a deletional mutation of 182 bp with an **out**-of-**frame** premature stop codon in the extra-cellular domain of G-CSFR. The deletion occurs between position 1128 and 1310, involving exons 8-10. Cysteine residues required for disulfide linkage and dimerization are preserved. The region encoding the WSDWS motif is involved in the deletion, but the deduced amino acid sequence is WSDWG. A premature stop codon occurs corresponding to position 1404. **GFP**- and epitope-tagged constructs of wild-type and mutant G-CSFR were made and transfected into COS, 293, and Ba/F3 cells. Since no **GFP** or epitope-tagged mutant was found in the external environment, it is unlikely that the mutant G-CSFR exists as a soluble receptor that binds to natural or pharmacologic amounts of G-CSF. However, co-precipitation studies demonstrated an association of the wild-type receptor with mutant receptor, indicating that the dominant negative model of receptor signaling could occur. This association was independent of ligand binding. Subcellular localization by

confocal microscopy of **GFP**-tagged wild-type G-CSFR showed its presence in the endoplasmic reticulum and the cell surface, whereas the **GFP**-tagged mutant G-CSFR showed a different pattern with concentration in the perinuclear region and the trans-golgi network. Pulse-chase experiments are being done to determine wild-type and mutant G-CSFR turnover and apoptosis assays are being performed to determine the contibution of the mutant G-CSFR to the pathophysiology of neutropenia.

L10 ANSWER 7 OF 7 MEDLINE DUPLICATE 6
AN 2000202702 MEDLINE
DN 20202702 PubMed ID: 10737809
TI Random **GFP**::cDNA fusions enable visualization of subcellular structures in cells of Arabidopsis at a high frequency.
AU Cutler S R; Ehrhardt D W; Griffitts J S; Somerville C R
CS Carnegie Institution of Washington, Department of Plant Biology, 260 Panama Street, Stanford CA 94305, USA.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2000 Mar 28) 97 (7) 3718-23.
Journal code: 7505876. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-AF218816
EM 200004
ED Entered STN: 20000505
Last Updated on STN: 20000505
Entered Medline: 20000424
AB We describe a general approach for identifying components of subcellular structures in a multicellular organism by exploiting the ability to generate thousands of independent transformants in Arabidopsis thaliana. A library of Arabidopsis cDNAs was constructed so that the cDNAs were inserted at the 3' end of the **green fluorescent** protein (**GFP**) coding sequence. The library was introduced en masse into Arabidopsis by Agrobacterium-mediated transformation. Fluorescence imaging of 5,700 transgenic plants indicated that approximately 2% of lines expressed a fusion protein with a different subcellular distribution than that of soluble **GFP**. About half of the markers identified were targeted to peroxisomes or other subcellular destinations by non-native coding sequence (i.e., **out**-of-**frame** cDNAs). This observation suggests that some targeting signals are of sufficiently low information content that they can be generated frequently by chance. The potential of the approach for identifying markers with unique dynamic processes is demonstrated by the identification of a **GFP** fusion protein that displays a cell-cycle regulated change in subcellular distribution. Our results indicate that screening **GFP**-fusion protein libraries is a useful approach for identifying and visualizing components of subcellular structures and their associated dynamics in higher plant cells.

DUPLICATE 7

L13 ANSWER 13 OF 20 MEDLINE

AN 97001677 MEDLINE

DN 97001677 PubMed ID: 8844669

TI Isolation and expression of an open reading frame encoding sialidase from Trypanosoma rangeli.

AU Smith L E; Uemura H; Eichinger D

CS Department of Pathology, New York University School of Medicine, NY, USA.. smith101@mcrcr6.med.nyu.edu

NC 5 T32CA09161 (NCI)

SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1996 Jul) 79 (1) 21-33. Journal code: 8006324. ISSN: 0166-6851.

CY Netherlands

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

OS GENBANK-D50684; GENBANK-D50685; GENBANK-D50686; GENBANK-U46072; GENBANK-U46073; GENBANK-U46074

EM 199701

ED Entered STN: 19970219
Last Updated on STN: 19980206
Entered Medline: 19970129

AB Several protozoan parasites of human have been found to express enzymes capable of releasing terminal sialic acid residues from host glycans. These include enzymes similar in activity to bacterial and viral sialidases, as well as a novel type of enzyme, trans-sialidase, which can transfer sialic acid from one carbohydrate chain to another. Here we report the isolation of a gene and a gene fragment from the kinetoplastid Trypanosoma rangeli which encode products related in sequence to the trans-sialidase enzyme of T. **cruzi**. The gene fragment **ORF** is nearly identical to that of the complete gene, which encodes an enzymatically inactive protein. When the **ORF** of the gene fragment is fused to fragments from related genes, it encodes a product with sialidase activity. Both predicted T. rangeli protein products also have other potential structural features found in bacterial sialidases and in members of a previously described Trypanosoma trans-sialidase superfamily.